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Identification, characterization and mapping of EST-derived SSRs from cacao-*Ceratocystis cacaofunesta* interaction

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Ceratocystis cacaofunesta is an ascomycete responsible for the lethal wilt disease of cacao (*Theobroma cacao* L.). Marker-assisted selection combined with conventional breeding is one way in which the cacao resistance to Ceratocystis wilt can be improved. In this study, we screened a set of ESTs obtained from cacao elicited with *C. cacaofunesta* to identify EST-SSRs and test their efficacy for mapping. Among the 3,432 ESTs analyzed, 384 contained SSRs and 428 EST-SSRs were identified, mainly dinucleotides (78.5%), com 4 numbers of repeats (75.23%), and preferentially AG/CT motif (25.47%). GO function was assigned to the ESTs containing SSRs: 4.04% belonged to "defense response" category, with 20.69% of them to the sub-category "defense response to fungus". In relation to the ORF, the same amount of EST-SSRs was observed in 5'UTR as well as in the 3'UTR (about 30%). From the 428 EST-SSRs identified, 12 were polymorphic, revealing a total of 41 alleles. The number of alleles per locus ranged from 2 to 6, with an average of 3.41. Four EST-SSRs were mapped on the F_2 Sca 6 x ICS 1 population segregating for Ceratocystis wilt, which were distributed on the linkage groups 2, 3, 4 and 8. These markers contributed to saturate the genetic map of the cacao mapping population from CEPEC/CEPLAC and will be valuable for the research community to improve the cacao breeding program.

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